

SEQUENCE LISTING

<110> Julius, David J.
Caterina, Michael J.
Brake, Anthony J.

<120> Nucleic acid sequences encoding
capsaicin receptor and capsaicin receptor-related
polypeptides and uses thereof

<130> UCAL084CON

<140> Unassigned

<141> 2001-10-15

<150> 09/235,451

<151> 1999-01-22

<150> 60/072,151

<151> 1998-01-22

<150> 08/915,461

<151> 1997-08-20

<160> 48

<170> FastSEQ for Windows Version 4.0

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<211> 2880

<212> DNA

<213> R. rattus

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SECRET

6

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LOCUS: 000250

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SECRET

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105101 6060/60

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Arg Thr Phe Ile Met Thr Ile Gly Glu Phe Ser Val Leu Tyr Arg Glu
 1          5          10          15
Met Ser Ala Cys Asp Asn Phe Trp Met Lys Trp Ile Gly Lys Leu Ile
          20          25          30
Phe Val Ile Phe Glu Thr Phe Val Ser Ile Leu Gln Phe Asn Leu Leu
          35          40          45
Ile Ala Met Met Thr Arg Thr Tyr Glu Thr Ile Phe Leu
          50          55          60

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<210> 20
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(350)
 <223> n = A,T,C or G

<400> 20

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aggaaagctg	gattttggga	gcgggctgcc	tcccatggag	tcacagttcc	agggcgagga	180
ccggaattc	gccctcaga	taagagtcaa	cctcaactac	cgaaagggaa	caggtgccag	240
tcagccggat	ccaaaccgat	ttgaccgaga	tcggtctctc	aatgcggtct	cccggggtgt	300
ccccgaggat	ctggctggac	ttccagagta	cctgagcaag	accagcaagt		350

<210> 21
 <211> 764
 <212> DNA
 <213> Homo sapiens

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tcctgcatgc	cctagtgatg	atctcggaca	actcagctga	gaacattgca	ctggtgacca	180
gcatgtatga	tgggctctc	caagctgggg	ccgcctctg	ccctaccgtg	cagcttgagg	240
acatccgcaa	cctgcaggat	ctcacgcctc	tgaagctggc	cgccaaggag	ggcaagatcg	300
rratyttcaa	ggcacatcct	tgcaagcggg	aagttttcag	gactgaagcc	accttttccc	360
cgaaagtcca	ccgagtgggtg	gctaattggg	cctgtccggg	ttgtcgtgtg	aatgacctgg	420
gctttctgtg	gacagctgtg	aggagaactc	agtgtgrr	atcattgcct	ttcatttgca	480
aragcccgc	cgacaccgaa	tggtcgtttt	ggagcccctg	aacaaactgc	tgaggcgaa	540
atgggatctg	ctcatcccca	agttcttctt	aaacttcctg	tgtaattctga	ttacatgttc	600
atcttcaccg	ctgttgccca	ccatcagcct	accctgaaga	agcaggccgc	ccctcacctg	660
aaagcggagg	ttggaaactc	catgctgctg	acgggccaca	tccttatcct	gctagggggg	720
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<210> 22
 <211> 884
 <212> DNA
 <213> Homo sapiens

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ccacagagtc	agtgcagccc	atggagggac	aggaggacga	gggcaacggg	gcccagtaca	240
ggggatctct	ggwagcctcc	ttggagctct	tcaaattcac	catcggcctg	ggcgagctgg	300
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tgtcacctca	catcctgctg	ctcaacatgc	tcatcgccct	cwtgagcgag	accgtcaaca	420
gtgtcgccac	tgacagctgg	agcatctgga	agctgcagaa	agccatctct	gtcctggaga	480
tggagaatgg	ctattgggtg	tgaggaaga	agcagcgggc	aggtgtgatg	ctgacctgtg	540
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ggaggccaga	ggacagagca	gaggatcttt	ccaaccacat	ctgctggctc	tggggtccca	840
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<210> 23
 <211> 727

<212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(727)
 <223> Xaa = Any Amino Acid

<400> 23

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          20          25          30
Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg
          35          40          45
Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr
          50          55          60
Gly Ala Ser Gln Pro Asp Pro Asn Arg Phe Asp Arg Asp Arg Leu Phe
65          70          75          80
Asn Ala Val Ser Arg Gly Val Pro Glu Asp Leu Ala Gly Leu Pro Glu
          85          90          95
Tyr Leu Ser Lys Thr Ser Lys Tyr Leu Thr Asp Ser Glu Tyr Thr Glu
          100          105          110
Gly Ser Thr Gly Lys Thr Cys Leu Met Lys Ala Val Leu Asn Leu Lys
          115          120          125
Asp Gly Val Asn Ala Cys Ile Leu Pro Leu Leu Gln Ile Asp Arg Asp
          130          135          140
Ser Gly Asn Pro Gln Pro Leu Val Asn Ala Gln Cys Thr Asp Asp Tyr
          145          150          155          160
Tyr Arg Gly His Ser Ala Leu His Ile Ala Ile Glu Lys Arg Ser Leu
          165          170          175
Gln Cys Val Lys Leu Leu Val Glu Asn Gly Ala Asn Val His Ala Arg
          180          185          190
Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          195          200          205
Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Lys Gln Trp Asp Val
          210          215          220
Val Ser Tyr Leu Leu Glu Asn Pro His Gln Pro Ala Ser Leu Gln Ala
          225          230          235          240
Thr Asp Ser Gln Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ser
          245          250          255
Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met Tyr Asp Gly
          260          265          270
Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Asp
          275          280          285
Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala Ala Lys Glu
          290          295          300
Gly Lys Ile Xaa Ile Phe Xaa Arg His Ile Leu Ala Ser Gly Lys Phe
          305          310          315          320
Ser Gly Leu Lys Pro Pro Phe Pro Arg Lys Phe Thr Glu Trp Trp Leu
          325          330          335

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0397303-40334

Met Gly Pro Val Arg Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 355 360 365
 Pro Asp Arg His Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu
 370 375 380
 Gln Ala Lys Trp Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu
 385 390 395 400
 Cys Asn Leu Xaa Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln
 405 410 415
 Pro Thr Leu Lys Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly
 420 425 430
 Asn Ser Met Leu Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile
 435 440 445
 Tyr Leu Leu Val Gly Gln Lys Trp Lys Phe Trp Xaa Xaa Xaa Xaa Xaa
 450 455 460
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Pro Gly His Arg Val
 465 470 475 480
 Val Pro Ala Pro Ala Cys Val Cys Ala Gly Ala Gly Leu Ala Glu Pro
 485 490 495
 Ala Leu Leu Tyr Thr Trp Leu Pro Ala His Arg His Leu Gln Cys His
 500 505 510
 Asp Pro Glu Ala Leu Val Ser Leu Ser Gln Asp Trp Arg Pro Glu Ala
 515 520 525
 Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln Pro Met Glu Gly Gln
 530 535 540
 Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly Ile Leu Xaa Ala Ser
 545 550 555 560
 Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly Glu Leu Ala Phe Gln
 565 570 575
 Glu Gln Leu His Phe Arg Gly Met Val Leu Leu Leu Leu Leu Ala Tyr
 580 585 590
 Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met Leu Ile Ala Leu Xaa
 595 600 605
 Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser Trp Ser Ile Trp Lys
 610 615 620
 Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu Asn Gly Tyr Trp Trp
 625 630 635 640
 Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu Thr Val Gly Thr Lys
 645 650 655
 Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe Arg Val Glu Glu Val
 660 665 670
 Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr Leu Cys Glu Asp Pro
 675 680 685
 Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn Pro Val Leu Ala Ser
 690 695 700
 Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu Glu Asn Tyr Val Pro
 705 710 715 720
 Val Gln Leu Leu Gln Ser Asn
 725

caaggaggac aattaaaacg cttccttcat aagagcgggg atttatggaa aaaggccaaa
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2760
2820
2845

<210> 25
<211> 843
<212> PRT
<213> chicken

<400> 25
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20 25 30
Leu Glu Thr Ala Asp Asn Leu Gln Gly Thr Phe Ser Asn Lys Val Gln
35 40 45
Pro Ser Lys Ser Asn Ile Phe Ala Arg Arg Gly Arg Phe Val Met Gly
50 55 60
Asp Cys Asp Lys Asp Met Ala Pro Met Asp Ser Phe Tyr Gln Met Asp
65 70 75 80
His Leu Met Ala Pro Ser Val Ile Lys Phe His Ala Asn Met Glu Arg
85 90 95
Gly Lys Leu His Lys Leu Leu Ser Thr Asp Ser Ile Thr Gly Cys Ser
100 105 110
Glu Lys Ala Phe Lys Phe Tyr Asp Arg Arg Arg Ile Phe Asp Ala Val
115 120 125
Ala Arg Gly Ser Thr Lys Asp Leu Asp Asp Leu Leu Leu Tyr Leu Asn
130 135 140
Arg Thr Leu Lys His Leu Thr Asp Asp Glu Phe Lys Glu Pro Glu Thr
145 150 155 160
Gly Lys Thr Cys Leu Leu Lys Ala Met Leu Asn Leu His Asp Gly Lys
165 170 175
Asn Asp Thr Ile Pro Leu Leu Leu Asp Ile Ala Lys Lys Thr Gly Thr
180 185 190
Leu Lys Glu Phe Val Asn Ala Glu Tyr Thr Asp Asn Tyr Tyr Lys Gly
195 200 205
Gln Thr Ala Leu His Ile Ala Ile Glu Arg Arg Asn Met Tyr Leu Val
210 215 220
Lys Leu Leu Val Gln Asn Gly Ala Asp Val His Ala Arg Ala Cys Gly
225 230 235 240
Glu Phe Phe Arg Lys Ile Lys Gly Lys Pro Gly Phe Tyr Phe Gly Glu
245 250 255
Leu Pro Leu Ser Leu Ala Ala Cys Thr Asn Gln Leu Cys Ile Val Lys
260 265 270
Phe Leu Leu Glu Asn Pro Tyr Gln Ala Ala Asp Ile Ala Ala Glu Asp
275 280 285
Ser Met Gly Asn Met Val Leu His Thr Leu Val Glu Ile Ala Asp Asn
290 295 300
Thr Lys Asp Asn Thr Lys Phe Val Thr Lys Met Tyr Asn Asn Ile Leu
305 310 315 320
Ile Leu Gly Ala Lys Ile Asn Pro Ile Leu Lys Leu Glu Glu Leu Thr

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Asn	Lys	Lys	Gly	Leu	Thr	Pro	Leu	Thr	Leu	Ala	Ala	Lys	Thr	Gly	Lys														
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Ile	Gly	Ile	Phe	Ala	Tyr	Ile	Leu	Arg	Arg	Glu	Ile	Lys	Asp	Pro	Glu														
															355								360			365			
Cys	Arg	His	Leu	Ser	Arg	Lys	Phe	Thr	Glu	Trp	Ala	Tyr	Gly	Pro	Val														
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His	Ser	Ser	Leu	Tyr	Asp	Leu	Ser	Cys	Ile	Asp	Thr	Cys	Glu	Lys	Asn														
385																390								395			400		
Ser	Val	Leu	Glu	Ile	Ile	Ala	Tyr	Ser	Ser	Glu	Thr	Pro	Asn	Arg	His														
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Glu	Met	Leu	Leu	Val	Glu	Pro	Leu	Asn	Arg	Leu	Leu	Gln	Asp	Lys	Trp														
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Asp	Arg	Phe	Val	Lys	His	Leu	Phe	Tyr	Phe	Asn	Phe	Phe	Val	Tyr	Ala														
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Ile	His	Ile	Ser	Ile	Leu	Thr	Thr	Ala	Ala	Tyr	Tyr	Arg	Pro	Val	Gln														
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Lys	Gly	Asp	Lys	Pro	Pro	Phe	Ala	Phe	Gly	His	Ser	Thr	Gly	Glu	Tyr														
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Phe	Arg	Val	Thr	Gly	Glu	Ile	Leu	Ser	Val	Leu	Gly	Gly	Leu	Tyr	Phe														
															485								490			495			
Phe	Phe	Arg	Gly	Ile	Gln	Tyr	Phe	Val	Gln	Arg	Arg	Pro	Ser	Leu	Lys														
															500								505			510			
Thr	Leu	Ile	Val	Asp	Ser	Tyr	Ser	Glu	Val	Leu	Phe	Phe	Val	His	Ser														
															515								520			525			
Leu	Leu	Leu	Leu	Ser	Ser	Val	Val	Leu	Tyr	Phe	Cys	Gly	Gln	Glu	Leu														
															530								535			540			
Tyr	Val	Ala	Ser	Met	Val	Phe	Ser	Leu	Ala	Leu	Gly	Trp	Ala	Asn	Met														
545																550								555			560		
Leu	Tyr	Tyr	Thr	Arg	Gly	Phe	Gln	Gln	Met	Gly	Ile	Tyr	Ser	Val	Met														
															565								570			575			
Ile	Ala	Lys	Met	Ile	Leu	Arg	Asp	Leu	Cys	Arg	Phe	Met	Phe	Val	Tyr														
															580								585			590			
Leu	Val	Phe	Leu	Leu	Gly	Phe	Ser	Thr	Ala	Val	Val	Thr	Leu	Ile	Glu														
															595								600			605			
Asp	Asp	Asn	Glu	Gly	Gln	Asp	Thr	Asn	Ser	Ser	Glu	Tyr	Ala	Arg	Cys														
															610								615			620			
Ser	His	Thr	Lys	Arg	Gly	Arg	Thr	Ser	Tyr	Asn	Ser	Leu	Tyr	Tyr	Thr														
625																630								635			640		
Cys	Leu	Glu	Leu	Phe	Lys	Phe	Thr	Ile	Gly	Met	Gly	Asp	Leu	Glu	Phe														
															645								650			655			
Thr	Glu	Asn	Tyr	Arg	Phe	Lys	Ser	Val	Phe	Val	Ile	Leu	Leu	Val	Leu														
															660								665			670			
Tyr	Val	Ile	Leu	Thr	Tyr	Ile	Leu	Leu	Leu	Asn	Met	Leu	Ile	Ala	Leu														
															675								680			685			
Met	Gly	Glu	Thr	Val	Ser	Lys	Ile	Ala	Gln	Glu	Ser	Lys	Ser	Ile	Trp														
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Lys	Leu	Gln	Arg	Pro	Ile	Thr	Ile	Leu	Asp	Ile	Glu	Asn	Ser	Tyr	Leu														
705																710								715			720		
Asn	Cys	Leu	Arg	Arg	Ser	Phe	Arg	Ser	Gly	Lys	Arg	Val	Leu																

Ile Thr Pro Asp Gly Gln Asp Asp Tyr Arg Trp Cys Phe Arg Val Asp
740 745 750
Glu Val Asn Trp Ser Thr Trp Asn Thr Asn Leu Gly Ile Ile Asn Glu
755 760 765
Asp Pro Gly Cys Ser Gly Asp Leu Lys Arg Asn Pro Ser Tyr Cys Ile
770 775 780
Lys Pro Gly Arg Val Ser Gly Lys Asn Trp Lys Thr Leu Val Pro Leu
785 790 795 800
Leu Arg Asp Gly Ser Arg Arg Glu Glu Thr Pro Lys Leu Pro Glu Glu
805 810 815
Ile Lys Leu Lys Pro Ile Leu Glu Pro Tyr Tyr Glu Pro Glu Asp Cys
820 825 830
Glu Thr Leu Lys Glu Ser Leu Pro Lys Ser Val
835 840

<210> 26

<211> 135

<212> DNA

<213> Homo sapiens

<400> 26

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gtcttcatca tctgtctgct ggcctatgta attctcacct acatcctcct gctcaacatg 120
tttatcgctc tcatg 135

<210> 27

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> consensus

<400> 27

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<210> 28

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> consensus

<400> 28

catgatcaga gatcgcgata tgatcagaca tagtt 35

<210> 29

<211> 135

<212> DNA

<213> chicken

<400> 29
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 cttatagccc ttata 135

<210> 30
 <211> 135
 <212> DNA
 <213> chicken

<400> 30
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 cttatagccc taatg 135

<210> 31
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 31
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<210> 32
 <211> 17
 <212> DNA
 <213> Homo sapiens

<400> 32
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<210> 33
 <211> 2544
 <212> DNA
 <213> Homo sapiens

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 caagccccag ctctccacgg ccaagagccg caccggctc tttgggaagg gtgactcgga 180
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<210> 34
 <211> 839
 <212> PRT
 <213> Homo sapiens

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<400> 34
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Gln Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Asn Ser Arg
  20             25             30
Pro Pro Pro Ala Lys Pro Gln Leu Ser Thr Ala Lys Ser Arg Thr Arg
  35             40             45
Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro
  50             55             60
His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro
  65             70             75             80
Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu
  85             90             95
Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu
  100            105            110
Tyr Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln

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05070303-00000000

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130	135	140
Thr Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu		
145	150	155
Lys Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu		
165	170	175
Leu Leu Glu Ile Ala Arg Gln Thr Asp Ser Leu Lys Glu Leu Val Asn		
180	185	190
Ala Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile		
195	200	205
Ala Ile Glu Arg Arg Asn Met Ala Leu Val Thr Leu Leu Val Glu Asn		
210	215	220
Gly Ala Asp Val Gln Ala Ala His Gly Asp Phe Phe Lys Lys Thr		
225	230	235
Lys Gly Arg Pro Gly Phe Tyr Phe Gly Glu Leu Pro Leu Ser Leu Ala		
245	250	255
Ala Cys Thr Asn Gln Leu Gly Ile Val Lys Phe Leu Leu Gln Asn Ser		
260	265	270
Trp Gln Thr Ala Asp Ile Ser Ala Arg Asp Ser Val Gly Asn Thr Val		
275	280	285
Leu His Ala Leu Val Glu Val Ala Asp Asn Thr Ala Asp Asn Thr Lys		
290	295	300
Phe Val Thr Ser Met Tyr Asn Glu Ile Leu Ile Leu Gly Ala Lys Leu		
305	310	315
His Pro Thr Leu Lys Leu Glu Glu Leu Thr Asn Lys Lys Gly Met Thr		
325	330	335
Pro Leu Ala Leu Ala Ala Gly Thr Gly Lys Ile Gly Val Leu Ala Tyr		
340	345	350
Ile Leu Gln Arg Glu Ile Gln Glu Pro Glu Cys Arg His Leu Ser Arg		
355	360	365
Lys Phe Thr Glu Trp Ala Tyr Gly Pro Val His Ser Ser Leu Tyr Asp		
370	375	380
Leu Ser Cys Ile Asp Thr Cys Glu Lys Asn Ser Val Leu Glu Val Ile		
385	390	395
Ala Tyr Ser Ser Ser Glu Thr Pro Asn Arg His Asp Met Leu Leu Val		
405	410	415
Glu Pro Leu Asn Arg Leu Leu Gln Asp Lys Trp Asp Arg Phe Val Lys		
420	425	430
Arg Ile Phe Tyr Phe Asn Phe Leu Val Tyr Cys Leu Tyr Met Ile Ile		
435	440	445
Phe Thr Met Ala Ala Tyr Tyr Arg Pro Val Asp Gly Leu Pro Pro Phe		
450	455	460
Lys Met Glu Lys Thr Gly Asp Tyr Phe Arg Val Thr Gly Glu Ile Leu		
465	470	475
Ser Val Leu Gly Gly Val Tyr Phe Phe Phe Arg Gly Ile Gln Tyr Phe		
485	490	495
Leu Gln Arg Arg Pro Ser Met Lys Thr Leu Phe Val Asp Ser Tyr Ser		
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Glu Met Leu Phe Phe Leu Gln Ser Leu Phe Met Leu Ala Thr Val Val		
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[illegible]

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<211> 2380

<212> DNA

<213> Homo sapiens

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097303-04504

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<210> 36
 <211> 764
 <212> PRT
 <213> Homo sapiens

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 Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg
 35 40 45
 Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr
 50 55 60

Gly 65	Ala	Ser	Gln	Pro	Asp	Pro	Asn	Arg	Phe	Asp	Arg	Asp	Arg	Leu	Phe
Asn	Ala	Val	Ser	Arg	Gly	Val	Pro	Glu	Asp	Leu	Ala	Gly	Leu	Pro	Glu
Tyr	Leu	Ser	Lys	Thr	Ser	Lys	Tyr	Leu	Thr	Asp	Ser	Glu	Tyr	Thr	Glu
Gly	Ser	Thr	Gly	Lys	Thr	Cys	Leu	Met	Lys	Ala	Val	Leu	Asn	Leu	Lys
Asp	Gly	Val	Asn	Ala	Cys	Ile	Leu	Pro	Leu	Leu	Gln	Ile	Asp	Arg	Asp
Ser	Gly	Asn	Pro	Gln	Pro	Leu	Val	Asn	Ala	Gln	Cys	Thr	Asp	Asp	Tyr
Tyr	Arg	Gly	His	Ser	Ala	Leu	His	Ile	Ala	Ile	Glu	Lys	Arg	Ser	Leu
Gln	Cys	Val	Lys	Leu	Leu	Val	Glu	Asn	Gly	Ala	Asn	Val	His	Ala	Arg
Ala	Cys	Gly	Arg	Phe	Phe	Gln	Lys	Gly	Gln	Gly	Thr	Cys	Phe	Tyr	Phe
Gly	Glu	Leu	Pro	Leu	Ser	Leu	Ala	Ala	Cys	Thr	Lys	Gln	Trp	Asp	Val
Val	Ser	Tyr	Leu	Leu	Glu	Asn	Pro	His	Gln	Pro	Ala	Ser	Leu	Gln	Ala
Thr	Asp	Ser	Gln	Gly	Asn	Thr	Val	Leu	His	Ala	Leu	Val	Met	Ile	Ser
Asp	Asn	Ser	Ala	Glu	Asn	Ile	Ala	Leu	Val	Thr	Ser	Met	Tyr	Asp	Gly
Leu	Leu	Gln	Ala	Gly	Ala	Arg	Leu	Cys	Pro	Thr	Val	Gln	Leu	Glu	Asp
Ile	Arg	Asn	Leu	Gln	Asp	Leu	Thr	Pro	Leu	Lys	Leu	Ala	Ala	Lys	Glu
Gly	Lys	Ile	Glu	Ile	Phe	Arg	His	Ile	Leu	Gln	Arg	Glu	Phe	Ser	Gly
Leu	Ser	His	Leu	Ser	Arg	Lys	Phe	Thr	Glu	Trp	Cys	Tyr	Gly	Pro	Val
Arg	Val	Ser	Leu	Tyr	Asp	Leu	Ala	Ser	Val	Asp	Ser	Cys	Glu	Glu	Asn
Ser	Val	Leu	Glu	Ile	Ile	Ala	Phe	His	Cys	Lys	Ser	Pro	His	Arg	His
Arg	Met	Val	Val	Leu	Glu	Pro	Leu	Asn	Lys	Leu	Leu	Gln	Ala	Lys	Trp
Asp	Leu	Leu	Ile	Pro	Lys	Phe	Phe	Leu	Asn	Phe	Leu	Cys	Asn	Leu	Ile
Tyr	Met	Phe	Ile	Phe	Thr	Ala	Val	Ala	Tyr	His	Gln	Pro	Thr	Leu	Lys
Lys	Gln	Ala	Ala	Pro	His	Leu	Lys	Ala	Glu	Val	Gly	Asn	Ser	Met	Leu
Leu	Thr	Gly	His	Ile	Leu	Ile	Leu	Leu	Gly	Gly	Ile	Tyr	Leu	Leu	Val
Gly	Gln	Leu	Trp	Tyr	Phe	Trp	Arg	Arg	His	Val	Phe	Ile	Trp	Ile	Ser
Phe	Ile	Asp	Ser	Tyr	Phe	Glu	Ile	Leu	Phe	Leu	Phe	Gln	Ala	Leu	Leu

CGCGACCTGG AGTTCACTGA

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Thr Val Val Ser Gln Val Leu Cys Phe Leu Ala Ile Glu Trp Tyr Leu
              485              490              495
Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn Leu Leu Tyr
              500              505              510
Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val Met Ile Gln
              515              520              525
Lys Val Ile Leu Arg Asp Leu Leu Arg Phe Leu Leu Ile Tyr Leu Val
              530              535              540
Phe Leu Phe Gly Phe Ala Val Ala Leu Val Ser Leu Ser Gln Glu Ala
545              550              555              560
Trp Arg Pro Glu Ala Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln
              565              570              575
Pro Met Glu Gly Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly
              580              585              590
Ile Leu Glu Ala Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly
              595              600              605
Glu Leu Ala Phe Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu
              610              615              620
Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met
625              630              635              640
Leu Ile Ala Leu Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser
              645              650              655
Trp Ser Ile Trp Lys Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu
              660              665              670
Asn Gly Tyr Trp Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu
              675              680              685
Thr Val Gly Thr Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe
690              695              700
Arg Val Glu Glu Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr
705              710              715              720
Leu Cys Glu Asp Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn
              725              730              735
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 <213> Homo sapiens

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21

<210> 38
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SECRET

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			20					25					30		
Pro	Pro	Pro	Val	Lys	Pro	His	Ile	Phe	Thr	Thr	Arg	Ser	Arg	Thr	Arg
		35				40						45			
Leu	Phe	Gly	Lys	Gly	Asp	Ser	Glu	Glu	Ala	Ser	Pro	Leu	Asp	Cys	Pro
	50				55					60					
Tyr	Glu	Glu	Gly	Gly	Leu	Ala	Ser	Cys	Pro	Ile	Thr	Val	Ser	Ser	
65				70						75				80	
Val	Leu	Thr	Ile	Gln	Arg	Pro	Gly	Asp	Gly	Pro					
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